Fishpathogens.EU/NODA: A Free and Handy Online Platform for Betanodavirus Targeted Research and Data Sharing

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FISHPATHOGENS.EU/NODA: A FREE AND HANDY ONLINE PLATFORM FOR BETANODAVIRUS TARGETED RESEARCH AND DATA SHARING

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DATABASE PRESENTATION

Betanodaviruses are responsible for a severe neuropathological disease known as Viral Nervous Necrosis (VNN) that can affect a broad range of fish species worldwide. Betanodavirus genome consists of two single stranded positive sense RNA molecules, which are susceptible to reassortment events. The phylogenetic analysis of both genetic segments allowed the identification of at least four betanodavirus genotypes, namely RGNNV, SJNNV, BFNNV, TPNNV, as well as the two reassortants RGNNV/SJNNV and SJNNV/RGNNV. The infectivity of betanodavirus to an increasing number of fish species, its wide geographical extent and its economical and ecological impact, highlight the need of a platform for sharing epidemiological and molecular data.
Fishpathogens.eu is a website developed and maintained by the European Union Reference Laboratory for Fish Diseases (EURL-FISH). It has been previously launched for Viral Haemorrhagic Septicaemia (VHS) and Infectious Haematopoietic Necrosis (IHN), and have proven to be a valuable tool for experts targeted research. With the aim of collecting molecular and epidemiological information on betanodavirus, relevant for its control and research study, we extended FishPathogens.eu to also comprise VNN. The present database is going to be a useful tool to better understand betanodavirus diffusive dynamics and ecological features, as well as VNN epidemiology.

HOW CAN THE DATABASE BE ACCESSED?

- ✓ Login is required to upload and download information
- ✓ Everyone can register at www.fishpathogens.eu
- ✓ Without registering it is still possible to browse reports
- ✓ Everyone are encouraged to upload new reports

WHICH INFORMATION CAN BE UPLOADED?

Isolate information

- ✓ Sampling date
- ✓ Sample information
- ✓ Geographical location
- ✓ Water environment
- ✓ Host species
- ✓ Epidemiology information
- ✓ Laboratory source
- ✓ …

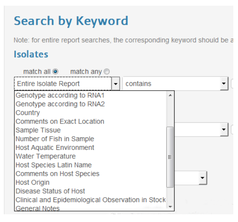
Sequence information

- ✓ Nucleotide sequence
- ✓ Gene region(s)
- ✓ Protein name(s)
- ✓ Sequencing method
- ✓ Basic annotation
- ✓ Genotype/Genogroup
- ✓ …

HOW TO RETRIEVE INFORMATION?

Search possibilities by...

- ✓ Gene region(s)
- ✓ Geographical location
- ✓ Keyword
- ✓ BLAST
- ✓ Sampling date
- ✓ …



Output

- ✓ .fasta sequences
- ✓ .csv (Excel)
- ✓ .kml (Google maps)
- ✓ .Newick (phylogenetic tree)

WHICH TOOLS ARE PROVIDED?

- ✓ New function!
- ✓ Sequence comparison using .fasta files
- ✓ Tree building using neighbour-joining
- ✓ Round or square phylogenetic trees
- ✓ Export in Newick format

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